

NiceZyme View of ENZYME: EC 3.2.1.23

Official Name

Beta-galactosidase.

Alternative Name(s)

Exo-(1->4)-beta-D-galactanase.

Lactase.

Reaction catalysed

Hydrolysis of terminal non-reducing beta-D-galactose residues in beta-D-galactosides Comment(s)

Some enzymes in this group hydrolyze alpha-L-arabinosides; some animal enzymes also hydrolyze beta-D-fucosides and beta-D-glucosides (cf. EC 3.2.1.108).

Human Genetic Disease(s)

Cangliosidosis,

generalized GM1, type MIM:230500

Gangliosidosis,

generalized GM1, type MIM:230600

Mucopolysaccharidosis MIM:253010 **IVB**

Cross-references

Biochemical Pathways;

map number(s)

PROSITE PDOC00495; PDOC00531; PDOC00910

BRENDA 3.2.1.23

PUMA2 3.2.1.23

PRIAM enzyme-

3.2.1.23 specific profiles

Kyoto University

LIGAND chemical 3.2.1.23

database

IUBMB Enzyme

3.2.1.23 Nomenclature

KFGG ENZYME: 3.2.1.23

Help

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EC
Entry
          3.2.1.23
                                    Enzyme
          beta-galactosidase;
Name
          lactase;
          beta-lactosidase;
          maxilact:
          hydrolact;
          beta-D-lactosidase;
          S 2107;
          lactozym;
          trilactase;
          beta-D-galactanase;
          oryzatym;
          sumiklat
Class
          Hydrolases
          Glycosidases
          Glycosidases, i.e. enzymes hydrolysing O- and S-glycosyl
          compounds
          beta-D-galactoside galactohydrolase
Sysname
          Hydrolysis of terminal non-reducing beta-D-galactose residues in
Reaction
          beta-D-galactosides
Other reac R01105 R01678 R01679 R03355 R03616 R04633 R04783 R05112 R05994
          R06010 R06098 R06099 R06111 R06144 R06202
           Some enzymes in this group hydrolyse alpha-L-arabinosides; some
Comment
          animal enzymes also hydrolyse beta-D-fucosides and
          beta-D-glucosides; cf. EC 3.2.1.108 lactase.
          PATH: map00052 Galactose metabolism
Pathway
          PATH: map00511 N-Glycan degradation
          PATH: map00531 Glycosaminoglycan degradation
          PATH: map00561 Glycerolipid metabolism
          PATH: map00600 Sphingolipid metabolism
          PATH: map00604 Glycosphingolipid biosynthesis - ganglioseries
          PATH: map01032 Glycan structures - degradation
Ortholog
          KO: K01190 beta-galactosidase
Genes
          HSA: 2720 (GLB1) 3938 (LCT)
          MMU: 12091(Glb1) 226413(Lct)
          RNO: 116569(Lct) 316033(Glb1_mapped)
          CFA: 403873 (GLB1)
          DME: CG9092-PA(CG9092)
          CEL: T19B10.3
          ATH: At1g72990(F3N23.19) At3g52840(F8J2.10) At5g20710(T1M15.110)
          CME: CMP078C
          DDI: DDB0188784
          ECO: b0344(lacZ) b3076(ebgA) b3077(ebgC)
          ECJ: JW0335(lacZ) JW3048(ebgC)
          ECE: Z0440(lacZ) Z4429(ebgA) Z4430(ebgC)
```

ECS: ECs0397 ECs3958 ECs3959

3:2:1-23



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ENZYME: 3.2.1.120

Help

EC Entry

3.2.1.120

Enzyme

Name

oligoxyloglucan beta-glycosidase;

isoprimeverose-producing oligoxyloglucan hydrolase;

oligoxyloglucan hydrolase

Class

Hydrolases Glycosidases

Glycosidases, i.e. enzymes hydrolysing O- and S-glycosyl

compounds

Sysname

oligoxyloglucan xyloglucohydrolase

Reaction Hydrolysis of 1,4-beta-D-glucosidic links in oligoxyloglucans so

to remove successive isoprimeverose (i.e.

alpha-xylo-1,6-beta-D-glucosyl-) residues from the non-reducing

chain ends

Reference 1 [PMID: 4019436]

Kato Y, Matsushita J, Kubodera T, Matsuda K.

A novel enzyme producing isoprimeverose from oligoxyloglucans of

Aspergillus oryzae.

J. Biochem. (Tokyo). 97 (1985) 801-10.

Other DBs IUBMB Enzyme Nomenclature: 3.2.1.120

ExPASy - ENZYME nomenclature database: 3.2.1.120

ERGO genome analysis and discovery system: 3.2.1.120

BRENDA, the Enzyme Database: 3.2.1.120

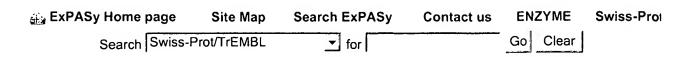
CAS: 97162-80-6

LinkDB

All OBs ;

=> Original format

DBGET integrated database retrieval system, GenomeNet



NiceZyme View of ENZYME: EC 3.2.1.120

Official Name

Oligoxyloglucan beta-glycosidase.

Alternative Name(s)

Isoprimeverose-producing oligoxyloglucan hydrolase.

Reaction catalysed

Hydrolysis of 1,4-beta-D-glucosidic links in oligoxyloglucans so as to remove successive isoprimeverose (i.e. alpha-xylo-1,6-beta-D-glucosyl-) residues from the non-reducing chain ends

Cross-references

BRENDA	3.2.1.120
PUMA2	3.2.1.120
PRIAM enzyme-specific profiles	3.2.1.120
Kyoto University LIGAND chemical database	3.2.1.120
IUBMB Enzyme Nomenclature	3.2.1.120
IntEnz	3.2.1.120
MEDLINE	Find literature relating to 3.2.1.120

MetaCyc 3.2.1.120

View entry in original ENZYME format

View entry in raw text format (no links)

All ENZYME / UniProtKB/Swiss-Prot entries corresponding to 3.2.1.-

All ENZYME / UniProtKB/Swiss-Prot entries corresponding to 3.2.-.-

All ENZYME / UniProtKB/Swiss-Prot entries corresponding to 3.-.-.

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